

Sequence: YGPVGRWLDNVRSGEBSLEQCBRFMGFDCTHOEVAVICSV 347

Query Match 100.0%; Score 1947; DB 22; Length 347;

Best Local Similarity 100.0%; Pred. No. 1.4e-153;

Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALLFSLIACTRPFASPGVYRVLVSGHCEGVVEVKQGWLGVCLDQWIKDVA 60

Db 1 malifsliaictrpfaspgvylvgqlhcegrevqkqwgtdvcdgwdikdav 60

Qy 61 LCPFLACGAASGTPGSLVYPPAKKEQVLYPSVCTSTPTEAACQEVEYDCSHDEDA 120

Db 61 lcpflacgaasgtpgslvypakkeqvlypsvctstpteaacqeveydcshdeda 120

Qy 121 GASENFESESSFSFEGVWIAUWIKKIFKEVEKHONWYTV-WT-WSTRAAKVVFQG 180

Db 121 gasefesessfsfegvwiawikkifkevekhonwytw-wt-wstraqkvvfqg 180

Qy 181 QGPVLDLKEWKAYSKKLUWMSMSSPFEATLWQPSWPKNNWNHFLTWVNEF 240

Db 181 caravitaqkcnkhaqriptiwlqmsasqreatiqlqdpstpwqkntnodedtwrced 240

Qy 241 PPDPLVYQINLCSPLFELVKHNYWGSVDTWQGEYFQDQVKQLGKSKSSPSFDPK 300

Db 241 pfdplvqinlcspfelfvkhnywgsvdtwqgeyfqdqvdkqlgkssspsfdpk 300

Qy 301 YGPVGRWLDNVRSGEBSLEQCBRFMGFDCTHOEVAVICSV 347

Db 301 ygpvgvglwldnvrsgesleqcbrfmgfdcthoevavicsv 347

Query Match 99.8%; Score 1943; DB 19; Length 347;

Best Local Similarity 100.0%; Pred. No. 3e-153; Mismatches 0; Indels 0; Gaps 0;

Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALLFSLILIACTRPFASPGVYRVLVYGGHCEGVVEVKQGWLGVCLDQWIKDVA 60

Db 1 malifslilialictrpfaspgvylvgqlhcegrevqkqwgtrddgwdikdav 60

Qy 61 LCPFLACGAASGTPGSLVYPPAKKEQVLYPSVCTSTPTEAACQEVEYDCSHDEDA 120

Db 61 lcpflacgaasgtpgslvypakkeqvlypsvctstpteaacqeveydcshdeda 120

Qy 121 GASENFESESSFSFEGVWIAUWIKKIFKEVEKHONWYTV-WT-WSTRAAKVVFQG 180

Db 121 gasefesessfsfegvwiawikkifkevekhonwytw-wt-wstraqkvvfqg 180

Qy 181 QGPVLDLKEWKAYSKKLUWMSMSSPFEATLWQPSWPKNNWNHFLTWVNEF 240

Db 181 caravitaqkcnkhaqriptiwlqmsasqreatiqlqdpstpwqkntnodedtwrced 240

Qy 241 PPDPLVYQINLCSPLFELVKHNYWGSVDTWQGEYFQDQVKQLGKSKSSPSFDPK 300

Db 241 pfdplvqinlcspfelfvkhnywgsvdtwqgeyfqdqvdkqlgkssspsfdpk 300

Qy 301 YGPVGRWLDNVRSGEBSLEQCBRFMGFDCTHOEVAVICSV 347

Db 301 ygpvgvglwldnvrsgesleqcbrfmgfdcthoevavicsv 347

RESULT 3

ID AAN68200 standard; Protein: 347 AA

AC AAN68200

XX

DT 07-DEC-1998 (first entry)



Jiang, D. Page 1  
09/19/02 4:22 10/14/8

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	1947	100.0		347	20	AYY13369		Amino acid sequence
2	1947	100.0		347	20	AYY13369		Human liver cell c
3	1943	99.8		347	19	AAW682400		Human scavenger receptor
4	1939	99.6		347	19	AAW64337		Human SRCA protein
5	721	37.0		1785	19	AAW6451		Human sbg14862SPER
6	719	36.9		442	22	AAE09446		Human sbg14862SPER
7	695	35.7		552	22	AAE09447		Human sbg14862SPER
8	691.5	35.5		1453	22	AAE6037		Human TANGO 234.
9	690	35.4		1319	22	AAE66040		Human TANGO 234 ex
10	690	35.4		1413	22	AAB66339		Human TANGO 234 ma
11	686	35.2		1121	22	ARM39493		Human polypeptide
12	686	35.2		1124	22	AAM41279		Human polypeptide
13	686	35.2		1124	22	AAM41280		Human polypeptide
14	686	35.2		1154	22	AAM3494		Human polypeptide
15	680	34.9		1120	22	AAU0396		Human secreted protein
16	669	34.4		821	22	AAU2709		Human full-length
17	663	34.1		1436	22	AAB66088		Bovine W1 protein
18	643	33.0		822	20	AAW90087		Human serine protein
19	643	33.0		875	20	AAW83361		Human neutrotrypsin
20	632	32.5		762	20	AAW90088		Mouse serine protease
21	632	32.5		761	20	AAW83362		Mouse neurotrypsin
22	582.5	29.9		1290	18	AAW01609		Rat von Ebner's 91
23	532.5	27.3		608	22	AAE11936		Human CG153 (or C5)
24	514	26.4		147	22	ABB2145		Human liver cell P
25	480	24.7		753	21	AAB00073		Human Lysyl oxidase
26	480	24.7		753	22	AAE11935		Amino acid sequence
27	478.5	24.6		573	21	AAG61903		Clone HOPEC84 #.
28	475	24.4		666	19	AAN64590		Human SCR protein
29	473	24.3		641	21	AAE11937		Human secreted protein
30	472	24.2		732	22	AAE11927		Human CG153 (or C5)
31	472	24.2		753	22	AAE11927		Human CG153 (or C5)
32	470.5	24.2		769	22	AAE11940		Human lipid metabolism
33	463.5	23.8		754	21	AAB60078		Murine Lysyl oxidase
34	453.5	23.3		774	21	AAB00077		Human Lysyl oxidase
35	452	23.2		757	21	ABB19127		Polypeptide islet
36	446.5	22.9		1186	22	ABB60992		Drosophila melanogaster
37	435	22.3		408	21	AAB51785		Human secreted protein
38	435	22.3		443	21	AAV72125		Peptide fragment #
39	435	22.3		443	21	AAV72125		Peptide fragment #
40	426.5	21.9		396	21	AAB651784		Protein fragment:
41	406.5	20.9		186	22	AAC253385		Gene 15 human secreted protein
42	345.5	17.7		225	22	AAM253317		Human protein sequence
43	319	16.4		280	21	AAE52444		Human Pancreatic cancer
44	315.5	16.2		136	22	AAG673568		Human Colon cancer
45	305.5	15.7		511	22	ABB66618		Drosophila melanogaster

## ALIGNMENTS

#

RESULT

1

AYY13369

standard:

Protein: 347 AA.

ID:

AYT13369

XX

AC:

AYY13369,

XX

DT:

25 JUN 1999 (first entry)

Amino acid sequence of protein FPF229.

DE

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KW

Secreted protein; transmembrane protein; human; enterocolitis;

congenital microvillus atrophy; skin disease; cell growth;

abnormal keratinocyte differentiation; psoriasis; epithelial cancer;

Parkinson's disease; Alzheimer's disease; ALS; neuropathy;

fibromodulin; dermal scarring; Usher Syndrome; anti-thrombotic;

wound healing; tissue repair.

XX

OS

Homo sapiens.

PN

W0991428-H2.

XX

FD

25-MAR-1999.

XX

PF

16-SEP-1998;

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PR

25-NOV-1997;

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17-SEP-1997;

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970S-0066840.

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970S-0059113.

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tein - protein search, using sw model

August 20, 2002, 12:57:10 ; Search time 32.8 seconds  
(without alignments)

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protein search, using sw model

August 20, 2002, 12:57:45, Search time: 23.07 seconds  
(without alignments)  
648 484 Million null updates/sec

US-09-904-462A-148  
1947 1 MAILSTLIACTRGPFLAS RMWGFHDCTHQDQDVAVICSV 347

bit score: 231628 seqs, 2425594 residues

gap table: BLOSUM62 Gapext 0.5

aligned:

al number of hits satisfying chosen parameters: 231628

minimum DB seq length: 0  
minimum DB seq length: 2000000000

post-processing: Minimum Match 0.8  
Maximum Match 100%

Listing first 45 summaries

database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5a\_COMB\_pep:\*
- 2: /cgn2\_6/ptodata/2/1aa/5b\_COMB\_pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6a\_COMB\_pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6b\_COMB\_pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/PRINS\_COMB\_pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/bas-filres\_FEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	Hit	Description
1	1938	99.5	346	3	US-09-04-916-2	Sequence 2, Appli	
2	721	37.0	1785	4	US-09-04-916-2	Sequence 3, Appli	
3	588	30.2	101	3	US-09-04-916-4	Sequence 4, Appli	
4	586	30.1	102	3	US-09-04-916-5	Sequence 5, Appli	
5	582.5	29.9	1290	1	US-09-04-916-2	Sequence 2, Appli	
6	553	28.4	101	3	US-09-04-916-3	Sequence 3, Appli	
7	480	24.7	753	4	US-09-04-916-2	Sequence 2, Appli	
8	480	24.7	752	4	US-09-04-916-2	Sequence 2, Appli	
9	475	24.4	666	4	US-09-04-916-2	Sequence 1, Appli	
10	463.5	23.8	754	4	US-09-04-916-8	Sequence 8, Appli	
11	463.5	23.8	754	4	US-09-04-916-8	Sequence 8, Appli	
12	453.5	23.3	754	4	US-09-04-916-3	Sequence 7, Appli	
13	453.5	23.3	774	4	US-09-04-916-2	Sequence 7, Appli	
14	285	14.6	100	3	US-09-04-916-15	Sequence 15, Appli	
15	282	14.5	100	3	US-09-04-916-17	Sequence 17, Appli	
16	279	14.3	100	3	US-09-04-916-10	Sequence 10, Appli	
17	266.5	13.7	100	3	US-09-04-916-11	Sequence 11, Appli	
18	260.5	13.4	495	2	US-08-04-916-7	Sequence 2, Appli	
19	260.5	13.4	495	4	US-09-04-916-7	Sequence 2, Appli	
20	260.5	13.4	520	2	US-08-04-916-15	Sequence 6, Appli	
21	260.5	13.4	520	4	US-09-04-916-6	Sequence 6, Appli	
22	258.5	13.3	451	1	US-08-04-916-2	Sequence 2, Appli	
23	254.5	13.1	101	3	US-09-04-916-9	Sequence 9, Appli	
24	252.5	13.0	451	1	US-08-04-916-12	Sequence 2, Appli	
25	252.5	13.0	451	2	US-08-04-916-22	Sequence 2, Appli	
26	252.5	13.0	451	2	US-08-04-916-2	Sequence 2, Appli	
27	252.5	13.0	451	2	US-08-04-916-18	Sequence 2, Appli	

RESULT 1  
US-09-034-916-2  
Sequence 2, Application US-09-034-916-16  
Patent No. 6046314

GENERAL INFORMATION:

APPLICANT: GEBE, JOHN A.  
APPLICANT: SIADAK, ANTHONY W.  
APPLICANT: ARIEFFO, ALEJANDRO A.  
TITLE OF INVENTION: SPALPHA, A NOVEL SCAVENGER RECEPTOR  
TITLE OF INVENTION: CYSTEINE-PITCH DOMAIN-CONTAINING POLYPEPTIDE AND MONOClonal  
TITLE OF INVENTION: ANTBULLES VHEKETU  
NUMBER OF SEQUENCES: 17

CHARACTERISTICS/ADDRESS:

ADDRESSEE: ROBINS & ASSOCIATES  
STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
CITY: MENLO PARK  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-09-034-916  
FILING DATE: 04-MAR-1998  
CLASSIFICATION: 536  
PCT/US APPLICATION DATA:

APPLICATION NUMBER: US-60-039-916  
FILING DATE: 06-MAR-1997  
ATTORNEY/AGENT INFORMATION:

NAME: POBINS, ROBERTA L.  
REGISTRATION NUMBER: 54,208  
REPRESENTATIVE NUMBER: 54,208

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 325-7812  
TELEFAX: (650) 325-7823

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 346 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-034-916-2

Query Match 92.9%, Similarity 100.0%, Pct. 27.7, Length 346;  
Best 152.5, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

